

Genetic diversity and antibiotic resistance of *Arcobacter butzleri* isolated from poultry and slaughterhouse environment in Portugal

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Arcobacter is considered an emerging enteric pathogen, commonly associated with diarrhea, abdominal pain and in some cases with bacteriemia. This genus is widely distributed, with fifteen species identified to date, of which the most common is *Arcobacter butzleri*. *Arcobacter* spp. has been isolated from environmental, animal, food and human samples, but poultry is considered its main reservoir. The extended use of antibiotics for disease control in modern food animal production, leads to a spread of resistant pathogenic bacteria, and *Arcobacter* spp. is no exception to this rule.

In this study, 43 *A. butzleri* isolates were obtained from poultry and environment samples at a Portuguese slaughterhouse, also three reference strains were included. All isolates were confirmed at species level by multiplex PCR; genomic DNA fingerprints of all isolates were determined using Pulsed Field Gel Electrophoresis (PFGE) after enzymatic digestion with SmaI. Resistance profiles to nine antibiotics were assessed by broth microdilution method.

Fifteen unique and 11 common PFGE fingerprints were identified among the 43 *Arcobacter* isolates studied, generating a total of 26 different PFGE fingerprints. This data demonstrates the high genetic diversity observed among *Arcobacter* isolates. Concerning the antibiotic susceptibility, all isolates tested were susceptible to gentamycin and one strain presented resistance to chloramphenicol. In contrast, 24 of the 43 isolates (55.8%) were resistant to ciprofloxacin. All the studied isolates presented resistance to multiple antibiotics simultaneously, especially to ampicillin, vancomycin, trimethoprim, piperacillin, cefoperazone and amoxicillin.

The results showed that *A. butzleri* isolated in Portugal presents a high genetic diversity, but also show high levels of resistance to several antimicrobial agents, this fact could represent a potential health hazard for humans through food chain contamination.